



## RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/824,322

Source: OIPE

Date Processed by STIC: 4/18/2001

**THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.**

**PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:**

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

**FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.**

**FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.**

**PATENTIN 2.1 e-mail help: [patin21help@uspto.gov](mailto:patin21help@uspto.gov) or phone 703-306-4119 (R. Wax)**

**PATENTIN 3.0 e-mail help: [patin3help@uspto.gov](mailto:patin3help@uspto.gov) or phone 703-306-4119 (R. Wax)**

**TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:**

### **Checker Version 3.0**

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

**Checker Version 3.0 can be down loaded from the USPTO website at the following address:**

**<http://www.uspto.gov/web/offices/pac/checker>**

OIPE

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/824,322

DATE: 04/18/2001

TIME: 16:32:27

Input Set : A:\PTO.txt

Output Set: N:\CRF3\04182001\I824322.raw

Does Not Comply

Corrected Diskette Needed

pp 2,4-6

3 <110> APPLICANT: Baker, Brenda  
 4 Bennett, C. Frank  
 5 Butler, Madeline M.  
 6 Shanahan, William R.  
 8 <120> TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE MODULATION OF TNF-a EXPRESSION  
 10 <130> FILE REFERENCE: ISPH-0501  
 12 <140> CURRENT APPLICATION NUMBER: US/09/824,322  
 13 <141> CURRENT FILING DATE: 2001-04-02  
 15 <150> PRIOR APPLICATION NUMBER: US 09/313,932  
 16 <151> PRIOR FILING DATE: 1999-05-18  
 18 <150> PRIOR APPLICATION NUMBER: US 09/166,186  
 19 <151> PRIOR FILING DATE: 1998-10-05  
 21 <160> NUMBER OF SEQ ID NOS: 503

## ERRORED SEQUENCES

23 <210> SEQ ID NO: 1  
 24 <211> LENGTH: 3634  
 25 <212> TYPE: DNA  
 26 <213> ORGANISM: Homo sapiens  
 28 <220> FEATURE:  
 29 <221> NAME/KEY: CDS  
 30 <222> LOCATION: (796..981,1589..1634,1822..1869,2171..2592)  
 W--> 31 <220> FEATURE:  
 32 <221> NAME/KEY: exon  
 33 <222> LOCATION: (615)..(981)  
 W--> 35 <220> FEATURE:  
 36 <221> NAME/KEY: intron  
 37 <222> LOCATION: (982)..(1588)  
 W--> 39 <220> FEATURE:  
 40 <221> NAME/KEY: exon  
 41 <222> LOCATION: (1589)..(1634)  
 W--> 43 <220> FEATURE:  
 44 <221> NAME/KEY: intron  
 45 <222> LOCATION: (1635)..(1821)  
 W--> 47 <220> FEATURE:  
 49 <221> NAME/KEY: exon  
 50 <222> LOCATION: (1822)..(1869)  
 W--> 52 <220> FEATURE:  
 53 <221> NAME/KEY: intron  
 54 <222> LOCATION: (1870)..(2070)  
 W--> 56 <220> FEATURE:  
 57 <221> NAME/KEY: exon  
 58 <222> LOCATION: (2171)..(3381)  
 60 <300> PUBLICATION INFORMATION:  
 61 <301> AUTHORS: Nedwin, G.E.

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Input Set : A:\PTO.txt

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62 Naylor, S.L.  
 63 Sakaguchi, A.Y.  
 64 Smith, D.  
 65 Jarrett-Nedwin, J.  
 66 Pennica, D.  
 67 Goeddel, D.V.  
 68 Gray, P.W.  
 69 <302> TITLE: Human lymphotoxin and tumor necrosis factor genes: structure, homology  
 70 and chromosomal localization  
 71 <303> JOURNAL: Nucleic Acids Res.  
 72 <304> VOLUME: 13  
 73 <305> ISSUE: 17  
 74 <306> PAGES: 6361-6373  
 75 <307> DATE: 1985-09-11  
 76 <308> DATABASE ACCESSION NO: X02910 Genbank  
 77 <309> DATABASE ENTRY DATE: 1997-02-17  
 79 <400> SEQUENCE: 1  
 81 gaattccggg tgatttcact cccggtctgc caggcttgct ctgctacccc acccagcctt 60  
 83 tectgaggcc tcaagcctgc caccaagccc ccagctcctt cccccgcag gacccaaaca 120  
 85 caggcctcag gactcaacac agcttttccc tccaaccctt tttctctccc tcaacggact 180  
 87 cagctttctg aagccctcc cagtctagt tctatctttt tctgcatcc tgtctggaag 240  
 89 ttagaaggaa acagaccaca gacctggtcc ccaaaagaaa tggaggcaat aggttttgag 300  
 92 gggcatggg acggggttca gctccaggg tctacacac aaatcagtc gtggcccaga 360  
 94 agacccccct cggaatcgga gcagggagga tggggagtgt gaggggtatc cttgatgctt 420  
 96 gtgtgtcccc aactttccaa atccccgccc ccgcgatgga gaagaaaccg agacagaagg 480  
 98 tgcagggccc actaccgctt cctccagatg agctcatggg tttctccacc aaggaagttt 540  
 100 tccgctgggt gaattattct tccccgccc tctctcgc ccagggacat ataaaggcag 600  
 102 ttgttgac acccagccag cagacgtcc ctcagcaagg acagcagagg accagctaag 660  
 104 agggagagaa gcaactacag accccccctg aaaacaaccc tcagacgcca cctccctga 720  
 106 caagctgcca ggcaggttct ctctctctca catactgacc cagggcttca cctctctctc 780  
 108 cctggaaagg acacc atg agc act gaa agc atg atc cgg gac gtg gag ctg 831  
 109 Met Ser Thr Glu Ser Met Ile Arg Asp Val Glu Leu  
 110 1 5 10  
 112 gcc gag gag gcg ctc ccc aag aag aca ggg ggg ccc cag ggc tcc agg 879  
 113 Ala Glu Glu Ala Leu Pro Lys Lys Thr Gly Gly Pro Gln Gly Ser Arg  
 114 15 20 25  
 116 cgg tgc ttg ttc ctc agc ctc ttc tcc ttc ctg atc gtg gca ggc gcc 927  
 117 Arg Cys Leu Phe Leu Ser Leu Phe Ser Phe Leu Ile Val Ala Gly Ala  
 118 30 35 40  
 120 acc acg ctc ttc tgc ctg ctg cac ttt gga gtg atc ggc ccc cag agg 975  
 121 Thr Thr Leu Phe Cys Leu Leu His Phe Gly Val Ile Gly Pro Gln Arg  
 122 45 50 55 60  
 W--> 124 gaa gag gtgagtgcct ggccagcctt catccactct cccacccaag gggaaatgag 1031 Glu Glu  
 E--> 126 agacgcaaga gagggagaga gatgggatgg gtgaaagatg tgcgctgata gggagggatg 1091  
 E--> 128 agagagaaaa aaacatggag aaagacgggg atgcagaaag agatgtggca agagatgggg 1151  
 E--> 130 aagagagaga gagaaagatg gagagacagg atgtctggca catggaaggt gctcactaag 1211  
 E--> 132 tgtgtatgga gtgaatgaat gaatgaatga atgaacaagc agatatataa ataagatatg 1271  
 E--> 134 gagacagatg tggggtgtga gaagagagat gggggaagaa acaagtgata tgaataaaga 1331  
 E--> 136 tggtagagaca gaaagagcgg gaaatatgac agctaaggag agagatgggg gagataagga 1391

insert  
 hard return

This  
 error  
 caused  
 remaining  
 sequence  
 next to be  
 in bold print

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Input Set : A:\PTO.txt

Output Set: N:\CRF3\04182001\I824322.raw

```

E--> 138 gagaagaaga tagggtgtct ggcacacaga agacactcag ggaaagagct gttgaatgct 1451
E--> 140 ggaaggtgaa tacacagatg aatggagaga gaaaaccaga cacctcaggg ctaagagcgc 1511
E--> 142 aggccagaca ggcagccagc tgttcctcct ttaaggggtga ctccctcgat gttaaccatt 1571
E--> 144 ctctttctcc ccaacag ttc ccc agg gac ctc tct cta atc agc cct ctg 1621
      145               Phe Pro Arg Asp Leu Ser Leu Ile Ser Pro Leu
W--> 146               65               70
E--> 147 gcc cag gca gtc agtaagtgtc tccaaacctc tttcctaatt ctgggtttgg 1673
      148 Ala Gln Ala Val
W--> 149               75
E--> 151 gtttgggggt agggtttagta ccggtatgga agcagtgggg gaaatttaaa gttttgtct 1733
E--> 153 tgggggagga tggatggagg tgaaagtagg ggggtatttt cttaggaagt taagggtctc 1793
E--> 155 agctttttct tttctctctc ctcttca gga tca tct tct cga acc ccg agt gac 1847
      156               Arg Ser Ser Ser Arg Thr Pro Ser Asp
W--> 157               80               85
E--> 159 aag cct gta gcc cat gtt gta ggtaagagct ctgaggatgt gtcttgggaac 1898
      160 Lys Pro Val Ala His Val Val
W--> 161               90
E--> 162 ttggagggct aggatttggg gattgaagcc cggctgatgg taggcagaac ttggagacaa 1958
E--> 164 tgtgagaagg actcgtgag ctcaagggaa ggggtggagga acagcacagg ccttagtggg 2018
E--> 166 atactcagaa cgctatggcc aggtgggatg tgggatgaca gacagagagg acaggaaccg 2078
E--> 168 gatgtggggg gggcagagct cgagggccag gatgtggaga gtgaaccgac atggccacac 2138
E--> 170 tgactctcct ctccctctct ccctccctcc a gca aac cct caa gct gag ggg 2190
      171               Ala Asn Pro Gln Ala Glu Gly
W--> 172               95               100
E--> 173 cag ctc cag tgg ctg aac cgc cgg gcc aat gcc ctc ctg gcc aat gcc 2238
      174 Gln Leu Gln Trp Leu Asn Arg Arg Ala Asn Ala Leu Leu Ala Asn Gly
W--> 175               105               110               115
E--> 177 gtg gag ctg aga gat aac cag ctg gtg gtg cca tca gag gcc ctg tac 2286
      178 Val Glu Leu Arg Asp Asn Gln Leu Val Val Pro Ser Glu Gly Leu Tyr
W--> 179               120               125               130
E--> 181 ctc atc tac tcc cag gtc ctc ttc aag ggc caa ggc tgc ccc tcc acc 2334
      182 Leu Ile Tyr Ser Gln Val Leu Phe Lys Gly Gln Gly Cys Pro Ser Thr
W--> 183               135               140               145
E--> 185 cat gtg ctc ctc acc cac acc atc agc cgc atc gcc gtc tcc tac cag 2382
      186 His Val Leu Leu Thr His Thr Ile Ser Arg Ile Ala Val Ser Tyr Gln
W--> 187               150               155               160
E--> 189 acc aag gtc aac ctc ctc tct gcc atc aag agc ccc tgc cag agg gag 2430
      190 Thr Lys Val Asn Leu Leu Ser Ala Ile Lys Ser Pro Cys Gln Arg Glu
W--> 191 165               170               175               180
E--> 193 acc cca gag ggg gct gag gcc aag ccc tgg tat gag ccc atc tat ctg 2478
      194 Thr Pro Glu Gly Ala Glu Ala Lys Pro Trp Tyr Glu Pro Ile Tyr Leu
W--> 195               185               190               195
E--> 197 gga ggg gtc ttc cag ctg gag aag ggt gac cga ctc agc gct gag atc 2526
      198 Gly Gly Val Phe Gln Leu Glu Lys Gly Asp Arg Leu Ser Ala Glu Ile
W--> 199               200               205               210
E--> 201 aat cgg ccc gac tat ctc gac ttt gcc gag tct ggg cag gtc tac ttt 2574
      202 Asn Arg Pro Asp Tyr Leu Asp Phe Ala Glu Ser Gly Gln Val Tyr Phe
W--> 203               215               220               225
E--> 205 ggg atc att gcc ctg tga ggaggacgaa catccaacct tcccaaaccg 2622

```

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Input Set : A:\PTO.txt

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206 Gly Ile Ile Ala Leu

W--&gt; 207 230

E--> 208 ctccccctgcc ccaatccctt tattaccccc tccttcagac accctcaacc tcttctggct 2682  
 E--> 210 caaaaagaga attgggggct tagggctcga acccaagctt agaactttaa gcaacaagac 2742  
 E--> 212 caccacttcg aaacctggga ttcaggaatg tgtggcctgc acagtgaagt gctggcaacc 2802  
 E--> 214 actaagaatt caaactgggg cctccagaac tcactggggc ctacagcttt gatccctgac 2862  
 E--> 216 atctggaatc tggagaccag ggagcctttg gttctggcca gaatgctgca ggacttgaga 2922  
 E--> 218 agacctcacc tagaaattga cacaagtgga ccttaggcct tctctctctc agatgtttcc 2982  
 E--> 220 agacttcctt gagacacgga gcccagccct ccccatggag ccagctccct ctatttatgt 3042  
 E--> 222 ttgcacttgt gattatttat tatttattta ttatttattt atttacagat gaatgtattt 3102  
 E--> 224 atttgggaga cgggggtatc ctgggggacc caatgtagga gctgccttgg ctcagacatg 3162  
 E--> 226 ttttccgtga aaacggagct gaacaatagg ctgttcccat gtagcccccct ggccctctgtg 3222  
 E--> 228 ccttcttttg attatgtttt ttaaaatatt tatctgatta agttgtctaa acaatgctga 3282  
 E--> 230 tttggtgacc aactgtcact cattgctgag cctctgctcc ccaggggagt tgtgtctgta 3342  
 E--> 232 atcgccctac tattcagtgg cgagaaataa agtttgotta gaaaagaaac atggtctcct 3402  
 E--> 234 tcttgggaatt aattctgcat ctgctctctc ttgtgggtgg gaagaagctc cctaagtcct 3462  
 E--> 236 ctctccacag gctttaagat ccctcggaac cagtcctcct cttagactcc tagggccctg 3522  
 E--> 238 gagaccctac ataaacaaag cccaacagaa tatcccccat cccccaggaa acaagagcct 3582  
 E--> 240 gaacctaat acctctccct cagggcctgg gaatttccaa ctctgggaat tc 3634

6100 &lt;210&gt; SEQ ID NO: 498

6101 &lt;211&gt; LENGTH: (20) 19 show

6102 &lt;212&gt; TYPE: DNA

6103 &lt;213&gt; ORGANISM: Artificial Sequence

6105 &lt;220&gt; FEATURE:

6106 &lt;223&gt; OTHER INFORMATION: Synthetic

6108 &lt;400&gt; SEQUENCE: 498

E--&gt; 6109 ctgattagag agaggtccc

6111 &lt;210&gt; SEQ ID NO: 499

6112 &lt;211&gt; LENGTH: (20) 18

6113 &lt;212&gt; TYPE: DNA

6114 &lt;213&gt; ORGANISM: Artificial Sequence

6116 &lt;220&gt; FEATURE:

6117 &lt;223&gt; OTHER INFORMATION: Synthetic

6119 &lt;400&gt; SEQUENCE: 499

E--&gt; 6120 ctgattagag agaggtcc

6144 &lt;210&gt; SEQ ID NO: 502

6145 &lt;211&gt; LENGTH: 20

6146 &lt;212&gt; TYPE: DNA

6147 &lt;213&gt; ORGANISM: Artificial Sequence

6149 &lt;220&gt; FEATURE:

6150 &lt;223&gt; OTHER INFORMATION: Synthetic

6152 &lt;400&gt; SEQUENCE: 502

E--&gt; 6153 caccaagctg cgggtcccca

6155 &lt;210&gt; SEQ ID NO: 503

6156 &lt;211&gt; LENGTH: 20

6157 &lt;212&gt; TYPE: DNA

6158 &lt;213&gt; ORGANISM: Artificial Sequence

6160 &lt;220&gt; FEATURE:

6161 &lt;223&gt; OTHER INFORMATION: Synthetic

(20) 19

(20) 18

20 ← insert cumulative  
 base total at right  
 margin of each line

see-  
 next page

## RAW SEQUENCE LISTING

DATE: 04/18/2001

PATENT APPLICATION: US/09/824,322

TIME: 16:32:28

Input Set : A:\PTO.txt

Output Set: N:\CRF3\04182001\I824322.raw

6163 &lt;400&gt; SEQUENCE: 503

E--&gt; 6164 tccgtcatcg ctcctcaggg

E--&gt; 6171 (6)

204 insert

*delete at end of file**see next page for more errors*

&lt;210&gt; 118

&lt;211&gt; 20

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;400&gt; 118

cccttcattc tcaaggcaca

*see item 12 on Enr Summary Sheet*

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/824,322

DATE: 04/18/2001

TIME: 16:32:29

Input Set : A:\PTO.txt

Output Set: N:\CRF3\04182001\I824322.raw

L:12 M:270 C: Current Application Number differs, Replaced Application Number  
 L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
 L:31 M:283 W: Missing Blank Line separator, <220> field identifier  
 L:124 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:8  
 L:126 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
 L:126 M:254 E: No. of Bases conflict, LENGTH:Input:1091 Counted:1035 SEQ:1  
 M:254 Repeated in SeqNo=1  
 L:146 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
 L:149 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
 L:157 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
 L:161 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
 L:172 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
 L:175 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
 L:179 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
 L:183 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
 L:187 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
 L:191 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
 L:195 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
 L:199 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
 L:203 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
 L:207 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
 L:240 M:252 E: No. of Seq. differs, <211>LENGTH:Input:3634 Found:3578 SEQ:1  
 L:970 M:283 W: Missing Blank Line separator, <220> field identifier  
 L:1271 M:283 W: Missing Blank Line separator, <220> field identifier  
 L:1420 M:283 W: Missing Blank Line separator, <220> field identifier  
 L:1869 M:258 W: Mandatory Feature missing, <220> FEATURE:  
 L:1869 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:  
 L:1869 M:283 W: Missing Blank Line separator, <400> field identifier  
 L:2411 M:283 W: Missing Blank Line separator, <220> field identifier  
 L:2712 M:283 W: Missing Blank Line separator, <220> field identifier  
 L:2946 M:283 W: Missing Blank Line separator, <220> field identifier  
 L:3180 M:283 W: Missing Blank Line separator, <220> field identifier  
 L:6109 M:254 E: No. of Bases conflict, LENGTH:Input:20 Counted:19 SEQ:498  
 L:6109 M:252 E: No. of Seq. differs, <211>LENGTH:Input:20 Found:19 SEQ:498  
 L:6120 M:254 E: No. of Bases conflict, LENGTH:Input:20 Counted:18 SEQ:499  
 L:6120 M:252 E: No. of Seq. differs, <211>LENGTH:Input:20 Found:18 SEQ:499  
 L:6153 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:20 SEQ:502  
 L:6164 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:20 SEQ:503  
 M:254 Repeated in SeqNo=503



# Raw Sequence Listing Error Summary

## ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER:

09/824,322

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 \_\_\_\_\_ Wrapped Nucleics      The number/text at the end of each line "wrapped" down to the next line.  
This may occur if your file was retrieved in a word processor after creating it.  
Please adjust your right margin to .3, as this will prevent "wrapping".
- 2 \_\_\_\_\_ Wrapped Aminos      The amino acid number/text at the end of each line "wrapped " down to the next line.  
This may occur if your file was retrieved in a word processor after creating it.  
Please adjust your right margin to .3, as this will prevent "wrapping".
- 3 \_\_\_\_\_ Incorrect Line Length      The rules require that a line not exceed 72 characters in length. This includes spaces.
- 4 \_\_\_\_\_ Misaligned Amino Acid      The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs  
Numbering      between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
- 5 \_\_\_\_\_ Non-ASCII      This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.  
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
- 6 \_\_\_\_\_ Variable Length      Sequence(s) \_\_\_\_\_ contain n's or Xaa's which represented more than one residue.  
As per the rules, each n or Xaa can only represent a single residue.  
Please present the maximum number of each residue having variable length and  
indicate in the (ix) feature section that some may be missing.
- 7 \_\_\_\_\_ PatentIn ver. 2.0 "bug"      A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid  
sequence(s) \_\_\_\_\_. Normally, PatentIn would automatically generate this section from the  
previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section  
to the subsequent amino acid sequence. This applies primarily to the mandatory <220>-<223>  
sections for Artificial or Unknown sequences.
- 8 \_\_\_\_\_ Skipped Sequences      Sequence(s) \_\_\_\_\_ missing. If intentional, please use the following format for each skipped sequence:  
(OLD RULES)      (2) INFORMATION FOR SEQ ID NO:X:  
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")  
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:  
This sequence is intentionally skipped  
  
Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
- 9 \_\_\_\_\_ Skipped Sequences      Sequence(s) \_\_\_\_\_ missing. If intentional, please use the following format for each skipped sequence.  
(NEW RULES)      <210> sequence id number  
<400> sequence id number  
000
- 10 \_\_\_\_\_ Use of n's or Xaa's      Use of n's and/or Xaa's have been detected in the Sequence Listing.  
(NEW RULES)      Use of <220> to <223> is MANDATORY if n's or Xaa's are present.  
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 11 \_\_\_\_\_ Use of "Artificial"      Use of "Artificial" only as "<213> Organism" response is incomplete, per 1.823(b) of New Sequence Rules.  
(NEW RULES)      Valid response is Artificial Sequence.
- 12   J   Use of <220>Feature      Sequence(s) 118 are missing the <220>Feature and associated headings.  
(NEW RULES)      Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial Sequence" or "Unknown"  
Please explain source of genetic material in <220> to <223> section.  
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)
- 13 \_\_\_\_\_ PatentIn ver. 2.0 "bug"      Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted  
file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).  
Instead, please use "File Manager" or any other means to copy file to floppy disk